<110 > CHOO, Yen

#### SEQUENCE LISTING

(1) CENERAL INFORMATION +

-(iii) NUMBER OF SEQUENCES+ 125

<2 0 > (2) INFORMATION FOR SEQ ID NO: 1:

SECURNCE CHARACTERISTICS: (A) LINOTH: 60 bace paire
(I) (B) TYPE: Bucleic soid
(C) STRANDEDNESS: single

<400> (xi) SEQUENCE DESCRIPTION: CEQ-ID NO: 1:

CTCCTGCAGT TGGACCTGTG CCATGGCCGG CTGGGCCGCA TAGAATGGAA

33

CAACTAAAGC

∠2/0> (2) INFORMATION FOR SEQ ID NO+ 2:

(1) SEQUENCE CHARACTERISTICS:

(2||>(A) LENGTH: 92 anino acido

(2||2|(B) TYPE: mino acido PRT (C) STRANDEDNESS :-(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

44007 (mi) SEQUENCE DESCRIPTION. SEQ ID NO: 2:

Met Ala Glu Glu Arg Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg

Ser Asp Glu Leu Thr Arg His Ile Arg Ile

His Thr Gly Gln Lys Pro Phe Gln Cys Arg

Ile Cys Met Arg Asn Phe Ser Xaa Xaa Xaa 45 50

Xaa Leu Xaa Xaa His Xaa Arg Thr His Thr

Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys 65 70

Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg 75

Lys Arg His Thr Lys Ile His Leu Arg Gln 85

Lys Asp

(2)07 -(2) INFORMATION FOR SEQ ID NO. 3:

(1) GEQUENCE CHARACTERISTICS.
(2) (A) LENGTH: 26 base-pairs
(2) (2) TYPE: Buoleic soid DNA (C) STRANDEDNESS: single (D) TOPOLOGY: linear -

<400>(xi) SEQUENCE DESCRIPTION: SEQ ID NO. 3:

TATGACTTGG ATGGGAGACC GCCTGG

KLUG, Auron SANCHEZ - GARCIA, Isidro <120> BINDING PROTEINS FOR RECOGNITION OF DNA 4130> 8325 - 2001.30 (GI-US3) 2140.7 lolo33,129 <141 > 2001 - 12-27

50 <150>08/793,408 60 <151> 1997-06-02 USO> PLT/6895/01949 2151 > 1995 -08-17 4160> 125 <170> PatentIn version3.2

<220> 4221 > MISC \_ FEATURE 42227 (48) ... (51) Xan = any amino acid Z2237 L220> 2221> MISC - FEATURE 1222> (53)...(54) 1223> Xaa = any avieno actol 12207 (231> MISC - FEATURE 12227 (5b) ... (5b) 4223> Xaa = any amino acid **42207** LZZI > HISC \_ FEATURE

```
(1) SEQUENCE CHARACTERICTICS:
               (C) STRANDEDNESS: single
                       (D)-TOPOLOGY:-linear
      ∠400> (*i) SEQUENCE DESCRIPTION SEQ ID NO. 4:
           AATTCCAGGC GGTCTCCCAT CCAAGTCA
                                                                                               28
<21<u>0≥ (2) INFORMATION FOR 6EQ ID NO+</u> 5:
             (1) ODQUENCE CHARACTERISTICS+

(2)|> (A) LEWSTH: 21 base pairs

(2)|> (B) TYPE+ nucloic soid

(C) STRANDERS
                       (C) STRANDEDNESS: Single (D) TOPOLOGY: Linear
    400> (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
           TATATAGCGT GGGCGTATAT A
                                                                                               21
<⊥|O> (2) INFORMATION FOR 6BQ-ID-NO+ 6:
              (i) SEQUENCE CHAPACTERISTICS:

(3) (A) LINGTH: 24 base pairs

(2) (B) TYPE: public soid-
(C) STRANDEDNESS: single
                       (D) TOPOLOGY: Linear
    (*1) SEQUENCE DESCRIPTION: OBQ ID NO: 6:
           GCGTATATAC GCCCACGCTA TATA
                                                                                               24
 <2|0> (2) INFORMATION FOR SEQ ID NO: 7:
             (i) SEQUENCE CHAPACTERISTICS:

22||> (A) LENGTH: 21 bass pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
                                                                                                     4220>
                                                                                                    2721> Misc - feature
                       (D) TOPOLOGY: linear
    Z400 > (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
           TATATAGCGN NNGCGTATAT A
<u><20> (2) INFORMATION FOR SEQ-ID NO•</u> 8:
                                                                                                     1221> ntec-feature
            (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH 24 base paire

(B) STRE- success cold DNA

(C) STRANDENRSS cold DNA

(D) TOPOLOGY: linear
                                                                                                      (223 > n is a, c, g ost
     1400 > (xi) SEQUENCE DESCRIPTION: SEQ ID NO. 8:
           GCGTATATAC GCNNNCGCTA TATA
<<u>≥10></u> -<del>(2) INFORMATION FOR CEQ ID NO+</del> 9:
              ∠400> (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
           TTCCATGGAG ACGCAGAAGC CCTTCAGCGG CCA
                                                                                                33
  ∠¾0> (2) INFORMATION FOR SEQ ID NO+ 10:
             (1) GEQUENCE CHARACTERISTICS:
```

```
-continued
```

```
(B) TYPE: nucleic acid-
                       (D) TOPOLOGY - linear
    2400 > (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
           TTCCATGGAG ACGCAGGTGA GTTCCTCACG CCA
                                                                                                   33
 ∠2/0≥ <del>(2) INFORMATION FOR CEQ ID NO.</del> 11:
              (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base paire

(B) TYPE: nucleic soid

(C) STRANDEDNESS: cingle

(D) TOPOLOGY: linear.
  ∠400> (#£) SEQUENCE DESCRIPTION SEQ ID NO. 11:
           CCCCTTTCTC TTCCAGAAGC CCTTCAGCGG CCA
                                                                                                   33
∠2/0≥ (2) INFORMATION FOR SEQ ID NO: 12:
               (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 anino acids
(2) (B) TYPE: amino acid PRT
(C) STRANDEDNESS:
                        (D) TOPOLOGY - unknown
                (11) MOLECULE TYPE+ poptide

∠408> (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

           Met Ala Glu Glu Lys Pro Phe Gln Cys Arg
5
           Ile Cys Met Arg Asn Phe Ser Asp Arg Ser
15
           Ser Leu Thr Arg His Thr Arg His Thr Gly
25 30
           Glu Lys Pro
 (1) SEQUENCE CHARACTERISTICS - CAUZ (A) LENGTH: 13 cmins acids PRT (C) STRANDEDNESS: (B) TOPOLOGY: unknown
                 (ii) MOLECULE TYPE: poptido
     <400> (xi) SEQUENCE DESCRIPTION SEQ ID NO. 13:
           Met Ala Glu Glu Lys Pro Phe Gln Cys Arg
           Ile Cys Met Arg Asn Phe Ser Glu Arg Gly
15 20
           Thr Leu Ala Arg His Glu Lye His Thr Gly 25
           Glu Lys Pro
∠2/0> (2) THFORMATION FOR SEQ ID NO: 14:
                (1) SEQUENCE CHARACTERISTICS+

2||2 (A) LENGTH: 27-amino coide-

2||2 (B) TITE: amino coid PRI

2||2 (C) SETANDERMISCH
                (C) TOPOLOGY - Linear
```

(ii) MOLECULE TYPE: poptide

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-continued
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∠400> (*i) SEQUENCE DESCRIPTION - SEQ ID NO+ 14:
           Phe Gln Cys Arg Ile Cys Met Arg Asn Phe
           Ser Gln Gly Gly Asn Leu Val Arg His Leu
15
           Arg His Thr Gly Glu Lys Pro
25
  <2/0> (2) INFORMATION FOR OBQ 10 NO. 15:
              (1) SEQUENCE CHARACTERISTICO:
(2) (A) LENCTH: 26 amino acido
(B) TYPE: amino acid PRT
(C) CTRANSBERGES
(D) TOPOLOGY: unknown
                (ii) - MOLECULE TYPE: peptide
    ∠400≥ (*i) SEQUENCE DESCRIPTION: SEQ TO NO. 15:
           Phe Gln Cys Arg Ile Cys Met Arg Asn Phe 5
           Ser Gln Ala Gln Thr Leu Gln Arg His Leu
15 20
           Lys His Thr Gly Glu Lys
25
<1/2> (2) INFORMATION FOR SEQ ID NO: 16:
              (4) SEQUENCE-CHARACTERISTICS:
(A) LENGTH: 26 emino acids
(B) TYPE: amino acid: PRT
(C) STRANBENNEGS:
(D) TOPOLOGY: unknown
                 (ii) MOLECULE TYPE: peptide
   ∠400> (x1) SEQUENCE DESCRIPTION: SEQ ID NO. 16:
           Phe Gln Cys Arg Ile Cys Met Arg Asn Phe 5
           Ser Gln Ala Ala Thr Leu Gln Arg His Leu
15 20
           Lys His Thr Gly Glu Lys
25
22/0> (3) INFORMATION FOR SEQ ID NO. 17:
              (1) SEQUENCE CHARACTERISTICS+

/2||/ (A) LENCTH: 26 emino soids

/2||/ (B) TIPE: amino soid PRT

(C) STRANDEDNESS+
(D) TOPOLOCY+ unknown
                (11) MOLECULE TYPE: poptido
     ∠400 > (*i) SEQUENCE DESCRIPTION SEQ ID NO. 17:
           Phe Gln Cys Arg Ile Cys Met Arg Asn Phe
5 10
           Ser Gln Ala Gln Asp Leu Gln Arg His Leu
15 20
           Lys His Thr Gly Glu Lys
<2/10> (2) INFORMATION FOR CBQ-ID-NO. 18:
```

```
(4) SEQUENCE CHARACTERISTICS+
(2) (A) LENGTH- 89 amino acid
(2) (B) TYPE: amino acid DRT
(C) STRANDEDNESS+
(D) TOPOLOGY+ unknown
```

-(ii) MOLECULE TYPE: protein

4400> (x1) SEQUENCE DESCRIPTION: SEQ 10 NO: 18:

Met Ala Glu Glu Lys Pro Phe Gln Cys Arg 5 10

Ile Cys Met Arg Asn Phe Ser Asp Arg Ser 15 20

Ser Leu Thr Arg His Thr Arg Thr His Thr 25

Gly Glu Lys Pro Phe Gln Cys Arg Ile Cys 35

Met Arg Asn Phe Ser Asp Arg Ser His Leu
45

Thr Arg His Thr Arg Thr His Thr Gly Glu 55

Lys Pro Phe Gln Cys Arg Ile Cys Met Arg 65 70

Asn Phe Ser Asp Arg Ser Asn Leu Thr Arg 75

His Thr Arg Thr His Thr Gly Glu Lys

∠2/0> (2) INFORMATION FOR CEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 emino coids

(B) TYPE: carino acid PR

(C) STRANDEDNESS:

(D) TODOLOGY: unknown

(11) WOLECULE TYPE: peptide

(x1) SEQUENCE DESCRIPTION - SEQ ID NO: 19:

Arg Ser Asp His Leu Thr Thr His Ile Arg
5 10

<u> 42/07 (2) INFORMATION FOR SEQ ID NO.</u> 20:

(1) SEQUENCE CHARACTERICTICS:

(A) LENGTH: 10 anino acids

(C) STRANDHONDES:

(B) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

2400 > (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Arg Val Asp Ala Leu Glu Ala His Arg Arg 5

∠2/0> (2) INFORMATION FOR SEQ-ID NO: 21:

(1) SEQUENCE CHARACTERISTICS (2) (A) LENGTH: 10 antino acids (B) TYPE: anino acids (C) STRANDEDNESS: (C) STRANDEDNESS: unknown

(ii) MOLECULE TYPE: poptide

```
∠400> (#4) CBQUBNOG BEGGREFTION CBQ ID NO+ 21:

           Gln Arg Ala Ser Leu Ala Ser His Met Arg
 <2/0> (2) INFORMATION FOR SEQ ID NO+ 22:
              (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acida.

(B) TYPE - mino acida.

(B) TYPE - mino acida.
                          (C) STRANDEDNESS:
                          (D) TOPOLOGY: unknown
                -(11) MOLECULE TYPE: poptide
    4400> (x1) SEQUENCE DESCRIPTION: SEQ-IB NO: 22:
           Asn Arg Asp Thr Leu Thr Arg His Ser Lys
  <u> ∠≥/0> (2) INFORMATION FOR #50 ID NO:</u> 23:
              (1) SEQUENCE CHARACTERISTICS+

(2) (A) LENGTH: 10 emino acide

(B) TIPE: emino acide

(C) GETAMPERMESC:

PRI
                         (C) STRANDEDNESS:
(D) TOPOLOGY: unknown-
                 (ii) MOLECULE TYPE: peptide
    ∠400> (*±) GEQUENCE DESCRIPTION+ GEQ ID NO+ 23:
           Gln Lys Gly His Leu Thr Glu His Arg Lys
∠2/0 > <del>(2) INFORMATION FOR CDQ ID NO+</del> 24:
                (i) SEQUENCE CHARACTERISTICS:
(2)/> (A) LENGTH: 10 amino acids
                (2)2>(8) TWPE: amino acid PRT
(0) ETRANDEDNESS:
(8) TOPOLOGY: unknown
                 (ii) MOLECULE TYPE: peptide
    ∠400> (wi) GEQUENCE DESCRIPTION: GDQ ID NO: 24:
            Gln Ser Val His Leu Gln Ser His Ser Arg

∠2/0><del>(2) INFORMATION FOR SEQ ID NO+</del> 25:

              (1) GEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acid
(B) TYPE: amino acid
(C) GYMANDENDEG:
(D) TOPOLOGY: unknown
                 (ii) MOLECULE TYPE: poptide
  ∠400> (#1) SEQUENCE DESCRIPTION SEQ. ID NO. 25:
            Arg Leu Asp Gly Leu Arg Thr His Leu Lys
5
∠2/0> (2) INFORMATION FOR SEQ ID NO. 26:
             (1)-SEQUENCE-CHARACTERISTICS:

(A) LENGTH: 10-amino-acide

(B) TYPE- amino-acide

(C) STRANDEDNESS:

(D) TOPOLOGY- unknown
```

(11) MOLECULE TYPE: poptide

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∠490 > (xi) SEQUENCE DESCRIPTION: SEQ ID NO+ 26:
         Thr Pro Gly Asn Leu Thr Arg His Gly Arg 5

∠≥ 0> (2) INFORMATION FOR SEQ ID NO+27:

               (i) SEQUENCE CHARACTERISTICS:
(2) (A) LENGTH: 10 amino acido
(2) 2 (B) TYPE: amino acid
                      (C) STRANDEDNESS:
                      -<del>(D) TOPOLOGY+ unkn</del>e
               (11) MOLECULE TYPE: peptide-
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO+ 27:
         Asn Gly Gly Asn Leu Gly Arg His Met Lys
5
∠2/0> (2) INFORMATION FOR SEQ ID NO. 28:
             (1) SEQUENCE CHARACTERISTICS:

(2) (A) LENGTH: 10 amino acide

(2) (C) STRANDEDMESS:

(C) STRANDEDMESS:
                      (D) TOPOLOGY: unknown
               (11) MOLEGULE TYPE: poptide
 400> (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:
          Arg Ala Asp Ala Leu Met Val His Lys Arg
5 10
∠2/0> (3) INFORMATION FOR SEQ ID NO+ 29:
               (i) SEQUENCE CHARACTERISTICS+

∠211≥(A) LENGTH: 10 amino acids
                      (B) TYPE: amino acid
                      (C) STRANDEDNESS:
               (14)-MOLECULD TYPE: peptide
  1400> (mi) GEQUENCE DESCRIPTION. SEQ TO NO. 29:
          Asn Gln Ser Asn Leu Glu Arg His His Arg
 ∠2/0 >(2) INFORMATION FOR SEQ ID NO: 30:
            (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acide

(A) TYPE: anino acide

(C) STRANBHONBOO:

(D) TOPOLOGY: unknown
             _(11) MOLECULE TYPE: peptide
     2460> (xi) GEQUENCE-DESCRIPTION: GEQ ID-NO+ 30:
          Asp Arg Ser Asn Leu Glu Arg His Thr Arg
5
42/0 > (2) INFORMATION FOR SEQ ID NO. 31:
              (A) LENGTH: 10 amino acide
              C2122 (B) TYPE amino acid PRI
                      (C) GTRANDEDNESS:-
```

(ii) MOLECULE TYDE: peptide

∠400> (x1) SEQUENCE DESCRIPTION SEQ ID NO: 31: Arg Ser Asp Thr Leu Lys Lys His Gly Lys 5 ∠2/0>-(2) ENFORMATION FOR SEQ ID NO: 32: (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH 10 amino soids

(2) (B) TYPB amino soid PRT (C) STRANDEDNESS: -{D}-TOPOLOGY+-unknown (11) MOLECULE TYPE: poptide ∠400> —(x±) ODQUENCE DESCRIPTION OF SEC NO+ 32: Gln Gln Ser Asn Leu Val Arg His Gln Arg
5 10 <u>⟨≥|0></u>(2) INFORMATION FOR SEQ ID NO. 33: (1) SEQUENCE CHARACTERISTICS+

(A) LENGUH: 10 amino acido

(B) TYPE amino acid

(C) STRANDEDNESS:

(C) DODOLOGY- Unknown (ii) MOLECULE TYRE: peptide ∠400> (wil) GEQUENCE DESCRIPTION: OBQ ID NO. 33: Asn Gly Ala Asn Leu Glu Arg His Arg Arg 5 <2|0>-(2) - INFORMATION FOR SEQ ED NO+ 34: (1) SEQUENCE CHARACTERISTICS: (C) STRANDEDNESS:
(D) TOPOLOGY: unknown (ii) MOLECULE TIPE: peptide ∠400> -(xi) sequence obscription: seq 10 No: 34: Arg Glu Asp Ala Leu Thr Ser His Glu Arg ∠2/0> <del>(2) INFORMATION FOR SEQ ID NO.</del> 35: (i) SEQUENCE CHARACTERISTICS: (C) STRANDEDNESS:

(D) TOPOLOGY unknown (11) MOLECULE TYPE: peptide 4400> -(\*4) SEQUENCE DESCRIPTION- SEQ ID NOT- 35: Arg Gly Asp His Leu Lys Asp His Ile Lys
5 10 ∠210 > (2) INFORMATION FOR SEQ ID NO. 36: (b) TOPOLOGY: unknown. (11) HOLDOULD TYPE: peptide

```
∠400>(mi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:
          Arg Gly Pro Asp Leu Ala Arg His Gly Arg
 ∠210> (2) INFORMATION FOR SEQ ID NO+ 37:
              (1) SEQUENCE CHARACTERISTICS:
(2) (A) LENGTH: 10 amino acido PR
                      (G) STRANDEDNESS:
                     (D) TOPOLOGY: unknown
              (ii) MOLECULE TYPE: poptide
    (x1)-SHQUBNOB DESCRIPTION- CEQ ID-No+ 37:
          Arg Glu Asp Val Leu Ile Arg His Gly Lys 5
 ∠2/0> (2) ENFORMATION FOR SEQ. ID NO. 38:
             (1) STRANDEDNESS:
             -(11) MOLECULE TYPE: poptide
    ∠400> (xi) SEQUENCE DESCRIPTION: SEQ ID NO. 38:
          Arg Ser Asp Leu Leu Gln Arg His His Lys
5
  ∠/o> (2) INFORMATION FOR SEQ ID NO+ 39:
               (i) SEQUENCE CHARACTERISTICS
             (B) TYPE+ amino acid
                      (C) STRANDEDNESS:
                     (D) TOPOLOGY: unknown
               (ii) MOLEGULE TYDE: peptide
    ∠460> (xi) SEQUENCE DESCRIPTION: GEQ 10 NO: 39:
          Arg Gln Asp Thr Leu Val Gly His Glu Arg
5
∠2/0> (2) INFORMATION FOR SEQ_ID_NO: 40:
              (a) tengra 10 anino acida 22|2 (b) TYPE: anino acida PRI (c) CTRANDEDNESS: (b) TOPOLOGY: unknown
              (ii) MOLECULE TYPE +- poptide
    (400> (*i) CEQUENCE DESCRIPTION: SEQ-ID-NO+ 40:
          Arg Ala Ala Asp Leu Asn Arg His Val Arg

⟨≥⟨o⟩ <del>⟨2⟩ INFORMATION FOR SEQ ID NO+</del> 41:

              (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:
                     (D) TOPOLOGY: unknown
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(44) MOLECULE TYPE: poptide

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1400 > (x1) SEQUENCE DESCRIPTION+ SEQ ID NO+ 41:
              Ser Gln Gly Asn Leu Gln Arg His Gly Arg
5

∠2/0>
-(2) INFORMATION FOR CEQ ID NO+ 42:

                  (i) GEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acid

(B) TYPE: amino acid
                           (C) STRANDEDNESS:
(D) TOPOLOGY: unknown
                   (ii) MOLECULE TYPE: poptide-
      (400) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:
              Thr Gly Gly Ser Leu Ala Arg His Glu Arg
5 10
  <2|O> (2) INFORMATION FOR SEQ-ID-NO+ 43:
                   (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acide
(2) (B) TYPEs amino acid
                            (C) GTRANDEDNESS:
                          (D) TOPOLOGY: unknown
                   (ii) MOLECULE-TYPE: peptide-
       <u>∠400>-(x1)-GEQUANCE DESCRIPTION: SEQ-ID NO:</u> 43:
              Asp His Ala Asn Leu Ala Arg His Thr Arg
 <2/10> (2) INFORMATION FOR CEQ ID-NO: 44:
                   (1) SEQUENCE CHARACTERISTICS:

(2) (A) LENGTH: 10 anino cold
(3) TYPE - amino cold
(5) - OTRANDEDNESS -
(D) TOPOLOGY: unknown
                  -(ii) MOLECULE TYPE -- peptide
     ∠400> -(*1) SEQUENCE DESCRIPTION: SEQ ID NO: 44:
              Leu Gln Ser Asn Leu Val Arg His Gln Arg

∠ ≥ PO → (3) INFORMATION FOR SEQ ID NO. 45:

                  (i) SEQUENCE CHARACTERISTICS:

22|>-(A) LENGTH: 10 anino soids
22|>-(B) TYPD: anino acid
(C) STRANDEDNESS:
                           (D) TOPOLOGY: unknown
                   (11) MOLECULE TYPE: peptide
    ∠400> (x1) SEQUENCE DESCRIPTION: SEQ 10 NO+ 45:
              Arg Lys Asp Val Leu Val Ser His Val Arg
5
∠ 20> -(2) INFORMATION FOR SEQ ID NO+ 46:
                   (i) SEQUENCE CHARACTERISTICS +

(ii) 14) LENGTH: 10 anino soids

(ii) TYPE: amino soid

(ii) TYPE: amino soid
                           (D)-TOPOLOGY+ unknown
                  -(ii)-MOLECULE TYPE: peptide
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<400 > (xi) SEQUENCE DESCRIPTION: SEQ TO NO: 46:
              Arg Arg Asp Val Leu Met Asn His Ile Arg

∠2/0> (2) INFORMATION FOR SEQ ID NOT 47:

                    (1) ORQUENCE CHARACTERICTICS+
(A) LENGTH: 10 amino acids
2/2 (B) TVPB: amino acid
                            (C) OTRANDEDNESS+
                            (D) TOPOLOGY - unknown
                    (11) MOLECULE TYPE: peptide.
         (400) (*1) SEQUENCE DESCRIPTION - SEQ ID NO: 47:
              Gln Gly Gly Asn Leu Val Arg His Leu Arg
  (1) SEQUENCE CHARACTERISTICS:

(2) (A) LENGTH: 10 amino acide

(B) TYPE: amino acid PRT

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown
                    (ii) MOLECULE TYPE: peptide
       ∠400> (x1) SEQUENCE DESCRIPTION - SEQ ID NO. 48:
              Ser Arg Asp Val Leu Arg Arg His Asn Arg
5 10
<u>∠210></u> <del>(2) INFORMATION FOR SEQ ID NO</del>: 49:
                   (1) SEQUENCE CHARACTERISTICS:

| | | (A) LENGTH: 10 amino acids

| (2) | (B) TYPE: amino acid | PR |
                            (C) STRANDEDNESS:
                            (D) TOPOLOGY: unknown
                   (11) MOLECULE TYPE: poptide
      2400> (wi) SEQUENCE DESCRIPTION+ SEQ-ID-NO+ 49:
              Glu Lys Ala Thr Leu Ala Arg His Met Lys
  <2/0> (2) INFORMATION FOR SEQ ID NO: 50:
                   (1) SEQUENCE CHARACTERISTICS:

(N) (A) LENGTH: 10 amino acide PRT

(12) (D) TIPD: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown
                 -(11) HOLECULE TYPE: peptide-
     ∠400> (xi) SEQUENCE DESCRIPTION: SEQ ID NO. 50:
              Gln Ala Gln Thr Leu Gln Arg His Leu Lys 5 10
∠2/0> -(2) INFORMATION FOR SEQ ID NO. 51:
                  (1) SPOUBNOS CHARACTERISTICS:

(2) (A) LENGTH+ 10 anino acids

(2) (B) TYPE: amino acid

(C) STRANDEDNESS:
                           (D) TOPOLOGY - unknown
                  -(11) MOLECULE TYPE: peptide
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∠400> (*±) SEQUENCE DESCRIPTION SEQ ID NO+ 51:
           Ile Ala Ser Asn Leu Leu Arg His Gln Arg

∠2/0> (3) INFORMATION FOR SEQ ID NO+ 52:

                 (i) SEQUENCE CHARACTERISTICS.

2012 (A) LENGTH: 10 mine sold

2012 (R) TYPE: smine sold

PLI
                       (C) STRANDEDNESS:
                       (D) TOPOLOGY: unk
                (11) MOLECULE TYPE: -popeldo
  1400> (xi) SEQUENCE DESCRIPTION: SEQ. ID NO. 521
           Arg Gly Asp His Leu Lys Asp His Ile Lys
5

∠2/0> (3) INFORMATION FOR SEQ 1D NO. 53:

              (1) OFQUENCE CHARACTERISTICS:

(A) LENGTH: 10 emine solde

(B) TYPE: smine sold PRT
                       (C)-STRANDEDNESST
                       (D) TOPOLOGY - unkr
                (ii) MOLECULE TYPE: poptide
     400 (x1) SEQUENCE DESCRIPTION: SEQ. ID NO. 53:
           Arg Ser Asp His Leu Thr Thr His Ile Arg
 <u>∠10></u> (2) INFORMATION FOR SEQ ID NO: 54:
             (1) SEQUENCE CHARACTERISTICS:

(2) -(A) -LENGTH: 10 -amino acids
             (2) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPODOGY: unknown
               -(11) MOLECULE TYPE: -poptido
   ∠400> (wi) SEQUENCE DESCRIPTION. SEQ ID NO: 54:
           Gln Leu Ala His Leu Ser Thr His Lys Arg
(2) (2) INFORMATION FOR SEQ. ID NO. 55:
               SEQUENCE CHARACTERISTICS:
                212 >(B) TYPE+ onine soid
                       (C) STRANDEDNESS:...
                (ii) MOLECULE-TYPB: peptide
   ∠400> (#1) CEQUENCE DESCRIPTION - SEQ ID NO. 55:
           Gln Ser Val His Leu Gln Ser His Ser Arg
5 10
 ∠2/0> +3) INFORMATION FOR SEQ ID NO: 56:
                (4) SEQUENCE CHARACTERISTICS:

(2) | (4) - LENGTH: 10 amino acids

(6) - TYPE+ amino acid-
(6) - OTRANDEDNESC+
                       (D) TOPOLOGY: unknown
                (11) HOLECULE TYPE: peptide-
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∠400≥ (xi)-GEQUENCE DESCRIPTION: GEQ ID NO: 56:
           Gln Lys Gly His Leu Thr Glu His Arg Lys
 2210> (2) INFORMATION FOR 6BQ ID NO: 57:
                (1) SEQUENCE CHARACTERISTICS.
                (2)(>(A) LENGTH: 10 amino acids
                (c) STRANDEDNESS:
                      (D) TOPOLOGY: unknown
              -(11) MOLECULE TYPE: peptide
     ZUOD≥ (*i) SEQUENCE DESCRIPTION - SEQ ID NO: 57:
          Gln Gly Gly Asn Leu Val Arg His Leu Arg
5
 <u>⟨2|0⟩</u> <del>(2) INFORMATION FOR ORQ ID NO+</del> 58:
               (1) SEQUENCE CHARACTERISTICS+

(2) (A) LENGTH: 10 -anino soids

(2) (B) TYPE: -anino soid

(C) STRANGENESC+
                      (D)-TOPOLOGY: unknown-
               (ii) MOLECULE TYPE: peptide
    4002 (*1) SEQUENCE DESCRIPTION: SEQ 10 NO. 58:
           Asn Gly Gly Asn Leu Gly Arg His Met Lys
∠2/0> (2) INFORMATION FOR SEQ ID NO.4 59:
                (i) GEQUENCE CHARACTERISTICST

| Z|| Z (A) LENGTH: 10 amino acida

| Z|| Z (B) TYPE: amino acid PRI
                      (C) STRANDEDNESS:
                    (D) TOPOLOGY: unknown-
               (ii) MOLECULE TYPE+ peptido-
   < 400> (xi) SEQUENCE DESCRIPTION: SEQ ID NO. 59:
           Ala Arg Ser Asn Leu Leu Arg His Thr Arg
 ∠2/0> (3) INFORMATION FOR CBQ ID NO: 60:
               (i) SEQUENCE CHARACTERISTICS:
               (C) STRENDEDNESS:
(D) TOPOLOGY: unknown
               (ii) MOLECULE TYPE: peptide
    ∠400> -(x1) SEQUENCE DESCRIPTION - GEQ-10 NO+ 60:
           Leu Gln Ser Asn Leu Val Arg His Gln Arg
(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino soids

(C) STRANDEDNESS:

(C) STRANDEDNESS:
                      (D) TOPOLOGY - unknown-
```

(ii) MOLECULE TYBE: peptide

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∠400> (wi) SEQUENCE DESCRIPTION - OBQ ID NO+ 61:
            Ile Ala Ser Asn Leu Leu Arg His Gln Arg

∠≥10> (3) INFORMATION FOR SEQ ID NO+ 62:

                 (1) SEQUENCE CHARACTERISTICS.
(2) (A) LENGTH 10 mino coids
(2) TIPB: caino coid PR
(C) STRANDEDNESS
                         (D) TOPOLOGY: unknown
                -(ii) MOLECULE TYPE: peptide
    1460> (wi) GEQUENCE DESCRIPTION: GEQ ID NO: 62:
            Asp Arg Ser Asn Leu Glu Arg His Thr Arg
5 10
 <210> <del>(2) INFORMATION FOR ORQ ID NO.</del> 63:
                 (1) CEQUENCE CHARACTERICULCS:

(A) LENGUH: 10 amino acido

(B) TYPE: amino acid
                         (D) TOPOLOGY: unknown.
                  (ii) MOLECULE TYPE: poptide
    ∠µ00≥ (xi) SEQUENCE DESCRIPTION SEQ ID NO. 63:
            Asn Gln Ser Asn Leu Glu Arg His His Arg
5
∠2/0> +2) INFORMATION FOR SEQ ID NO. 64:
                 (i) SIQUENCE CHARACTERISTICS:
(2) (A) LENGTH: 10 emino coid
(2) > (B) TYPE: emino coid
                         -(C) -STRANDEDNESS:
-(D) TOPOLOGY: unknown
                 -(ii)-MOLECULE TYPE:-poptide
 (x1) SEQUENCE DESCRIPTION - CBQ-IB NO+ 64:
            Gln Gln Ser Asn Leu Val Arg His Gln Arg
5 10
22/0> (2) INFORMATION FOR ORQ TO NOT 65:
              (a) ENGIN: 10 anino acid

(b) TYPE: amino acid

(c) STRANDEDNESS:
                        (D) TOPOLOGY: unknown
                 (11)-MOLECULE TYPE: peptide
 (41) SEQUENCE DESCRIPTION: SEQ 15 NOT 651
            Asn Gly Gly Asn Leu Gly Arg His Met Lys
2210> (2) INFORMATION FOR SEQ ID NOT 66:
                (1) SEQUENCE CHARACTERISTICS+
(2|) (A) LENCOH: 10 cmino soids
(2|2>(B) TYPE+ cmino soid PRI
(C) STRANDEDNESS1
                        -(D)-TOPOLOGY: unknown-
```

(ii) MOLECULE TYPE: poptide

4400> - (xi) SEQUENCE DESCRIPTION: SEQ-ID NO: 66: Asn Gly Ala Asn Leu Glu Arg His Arg Arg 5 10 ∠2/0> -(2) INFORMATION FOR SEQ ID NO. 67: (1) CEQUENCE CHARACTERISTICS:
(2) (A) LENGTH 10 anino solds
(2) (B) TYPE: amino sold PRT (C) STRANDBONESS: (D) TOPOLOGY: unknown -(11)-MOLEGULE-TYPE: -peptide-400> (x1) SEQUENCE DESCRIPTION: SEQ ID NO. 67: Ser Gln Gly Asn Leu Gln Arg His Gly Arg ∠2/0> (2) INFORMATION FOR SEQ ID NO+ 68: 21/2 (A) LENCEN: 10 amino acids
21/2 (B) TYPB: amino acid PRT
(C) STRANDEDNESS: (D) TOPOLOGY - unknown (ii) MOLECULE TYPE: peptido ∠400> (\*i) SEQUENCE DESCRIPTION: SEQ ID NO. 68: Ser His Pro Asn Leu Asn Arg His Leu Lys 5 ∠2/0> (2) INFORMATION FOR SEQ ID NO+ 69: (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 emino cold

(B) TYPE: amino cold PR (C) STRANDEDNESS:
(D) TOPOLOGY: unknown (ii) HOLECULE TYPE: poptide ∠460> (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69: Thr Pro Gly Asn Leu Thr Arg His Gly Arg <2|0> <del>(2) INFORMATION FOR SEQ ID NO.</del> 70: (1) SEQUENCE CHARACTERISTICS+

(2) (A) LENGTH: 10 unino acids 
(B) TYPEs unino acid PRI

(C) CTRANDENEGS:

(D) TOPOLOGY: unknown (11) MOLECULE TYPE: peptide 400> (xi) SEQUENCE DESCRIPTION: SEQ ID NOT 70: Asp Arg Ser Asn Leu Glu Arg His Thr Arg 5 ∠2/0> (2) INFORMATION FOR SEQ ID NO: 71: (1) SEQUENCE CHARACTERISTICS:-(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) -MOLECULE TYPE: populde.

<400> (x1) SEQUENCE DESCRIPTION SEQ ID NO+ 71: Asp His Ala Asn Leu Ala Arg His Thr Arg 5 ∠≥|0> (2) INFORMATION FOR OEQ ID NO: 721 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids ...

2/2×B) TYPE: amino acid... PRI (C) STRANDEDNESST (D) TOPOLOGY: unknown (11) MOLECULB TYPE: poptido-∠400> -(x1) GEQUENCE DESCRIPTION: GEQ\_ID\_NO: 72: Asp Arg Ser Ser Leu Thr Arg His Thr Arg ∠2/0> (2) INFORMATION FOR SEQ ID NO: 73: (1) CEQUENCE CHARACTERISTICS:
(2) (A) LENGER: 10 anino acido
(B) TYPE anino acid PRT
(C) STRANDEDNESS. (D) TOPOLOGY -- unknown--(44) MOLBOULE TYPE: poptide <u>∠400> (\*4) - SEQUENCE - DESCRIPTION+ SEQ ID NO:</u> 73: Glu Arg Gly Thr Leu Ala Arg His Glu Lys 5 10 (2) INFORMATION FOR SEQ 1D NO. 74: (i) GEQUENCE—CHARACTERISTICS:

(A) LENGTH: 10 mino acide

(B) TYPE: amino acid PAT

(C) OTRINDHONEGC:

(D) TOPOLOGY: unknown (ii) MOLECULE TYPE: peptide 1400> -(x1) SEQUENCE DESCRIPTION: GEQ ID NO+ 74: Asp Arg Arg Leu Leu Asp Arg His Gln Arg (2) (2) INFORMATION FOR SEQ ID NO. 75: (1) SEQUENCE CHARACTERISTICS:

(2)/(A) LENGTH: 10 amino solds

(B) TYPE: amino sold PR 7

(C) CTRANDEDNESS:

(D) TOPOLOGY: unknown -(11)-MOLECULE TYPE: peptide ∠400> (#±) GEQUENCE DESCRIPTION SEQ ID NO+ 75: Asp Arg Ser Ser Leu Thr Arg His Thr Arg 5 ∠2/0> (3) INFORMATION FOR SEQ ID NO. 76: (1) SEQUENCE CHARACTER ISTICS (2) (A) LENGTH: 10 emino acid (2) (B) TYPP: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: unknown

(ii) HOLEGULE TYPE: peptido

∠400> (mi) CEQUENCE DECORIPTION: SEQ ID NO+ 76: Glu Arg Thr Ser Leu Ser Arg His Ile Arg 5 10 ∠210> (3) INFORMATION FOR SEQ ID NO+ 77: (1) GEQUENCE CHARACTERISTICS:
(2) (A) LENGTH: 10 enine soids
(2) (2) (3) TYPD: amino soid PRI (C) STRANDEDNESS+ (D) TOPOLOGY: unknown (&&) MOLEGULE TYPE: poptide 1490 (xi) - SEQUENCE - DESCRIPTION: - CEQ ID NO. 77: Ser Ala Gly Thr Leu Val Arg His Ser Lys 5 <u>∠2/0> (3) INFORMATION FOR SEQ ID NO:</u> 78: (c) STRANDEDNESS:

(c) TOPOLOGY: unknown -(ii) MCLECULE TYDE: peptide-1400> (wi) CEQUENCE DESCRIPTION: CEQ ID NO: 78: Gln Ala Gln Thr Leu Gln Arg His Leu Lys 5 ∠2|0> <del>(2) INFORMATION FOR OBQ ID NO.</del> 79: (-i) - SEQUENCE CHARACTERISTICS:

(A) LENGTH+ 10 amino acid

(B) TYPE- amino acid

(C) - STRANDEDNESO
(D) TOPOLOGY- unknown (11) MODECULE TYPE: peptide 1490> (x1) SEQUENCE DESCRIPTION: SEQ ID NO+ 79: Glu Lys Ala Thr Leu Ala Arg His Met Lys ∠2/0> <del>(2) INFORMATION FOR SDQ-ID-NO:</del> 80: (1) SEQUENCE CHARACTERISTICS:

(2) (A) HENOTH: 10 mains acids

(C) TIPE: amins acid PRT

(C) STRANDEDNESS. (D) TOPOLOGY: unknown (ii) MOLBOULD TYPE: peptide 2.400> (mi) SEQUENCE DESCRIPTION - SEQ ID NO+ 80: Thr Gly Gly Ser Leu Ala Arg His Glu Arg 5 2)0>(2) INFORMATION FOR OBQ-10 NO+ 81: -(1)-SEQUENCE-CHARACTERISTICS:

(ii) NOLECULE TYPE: peptide

(2) (A) LENCTH: 10 mino acide
(B) TYPE: amino acid
(C) TYPE: Amino acid
(D) TYPE: Unknown

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4602 (NA) - SEQUENCE - DESCRIPTION - SEQ - ID NO+ 81:
             Arg Gln Ser Thr Leu Gly Arg His Thr Arg
   (2) (2) INFORMATION FOR SEQ-ID-NO+ 82:
                (4) CEQUENCE CHARACTERISTICO - (2) (3) LENGTH 10 andro acide (2) (3) TYPE - andro acid- PR
                         (G) -STRANDEDNESS:
                         -(D) TOPOLOGY: unknown
                  (11)-MOLECULE-TYPE:-peptido
       400> (x1) SEQUENCE DESCRIPTION SEQ 10-NO+ 82:
             Glu Lys Ala Thr Leu Ala Arg His Met Lys
5
 ∠2|0> <del>(2) INFORMATION FOR 6BQ ID NO.</del> 83:
                (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 mino acids

(B) TYPE: omino acid PRT

(C) STRANDEDNESS:
                         -(D) TOPOLOGY: unknown
                 -(11) MOLECULE TYPE: peptide
      ∠400> (xi) SEQUENCE DESCRIPTION: SEQ ID NO. 83:
             Gln Ala Gln Thr Leu Gln Arg His Leu Lys
5

∠2/0> - (2) INFORMATION FOR SEQ ID NO: 84:

                  (i) SEQUENCE CHARACTERISTICS:

(2) (A) LENGTHS 10 amino acids

(C) STRANDEDNESS:
                         -(D) TOPOLOGY: unknown-
                  (11) MOLECULE TYPE: poptide
     _(*i)-GEQUENCE DESCRIPTION: GEQ ID NO: 84:
             Glu Arg Gly Thr Leu Ala Arg His Glu Lys
∠≥/0> (3) INFORMATION FOR SEQ ID NO. 85:
                  (1) SEQUENCE CHARACTERICTICS+

(2) (A) LENGTH+ 10 amino anide
                  (C) TOPOLOGY unknown
                  -(ii) MOLECULE TYPE: poptide-
      <u>∠400></u> (xi) GEQUENCE DESCRIPTION: GEQ ID NO+ 85:
             Gly Arg Asp Ala Leu Ala Arg His Gln Lys
5

∠>|0> (2) INFORMATION FOR SEQ ID NO: 86:

                 (2) OBQUENCE CHARACTERISTICS:

(2) (B) TYPE: amino acid

(C) ETRANDEDNESS:
                        -(D) TOPOLOGY+ unknown-
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(ii) MOLECULE TYPE: peptide

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(400> (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 86:
             Arg Gly Pro Asp Leu Ala Arg His Gly Arg
5 10
   ∠210> (2) INFORMATION FOR CDQ ID NO. 87:
                 (4) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 anino acide
(B) TIPE: anino acid PRT
                         -(C) STRANDEDNESS+
                        -(D) TOPOLOGY: unknown
                  (11) MOLECULE TYPE: populde
      ∠400≥ -(xi) SEQUENCE DESCRIPTION: CEQ-ID NO. 87:
             Ser Arg Asp Val Leu Arg Arg His Asn Arg
  ∠∠10> (2) INFORMATION FOR SEQ 1D NO. 88:
                 (1) CDQUBNGE-CHARACTERISTICS+
(A) LENGTH: 10 amino-acido-
(B) TYPE- amino-acid-
(C) CTRANDEDNESS+
                        (D) TOPOLOCY+ unknown
                  -(11) MOLECULE TYPE: poptido
       ∠400> -(xi) - OEQUENCE - DESCRIPTION + SEQ -ID NO : 88:
             Arg Arg Asp Val Leu Met Asn His Ile Arg 5 10
∠≥|0> (2) INFORMATION FOR SEQ ID NO. 89:
                (1) CEQUENCE CHARACTERISTICS |

(2) | (A) LEMOTH: 10 mino acide

(B) TYPE: amino acide | FRT

(C) CTRANDEDNESS:
                         (D) TOPOLOGY - unknown
                  (ii) MOLECULE TYPE: peptide
    (wi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:
             Arg Lys Asp Val Leu Val Ser His Val Arg
 ∠2/0> (2) INPORMATION FOR SEQ ID NO. 90:
                (1) OF QUENCES CHARACTERISTICS:

(A) LENGTH: 10 cmino acide

(A) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown
                 (ii) MOLECULE TYPE: poptide
     1400> (x1) OBQUENCE DESCRIPTION: SEQ ID NO: 90:
           , Arg Arg Asp Val Leu Met Asn His Ile Arg 5 10
∠210≥ -(2) INFORMATION FOR CEQ ID NO: 91:
```

(±i-)-MOLECULE TYPE: poptide

2400> (x1) SEQUENCE DESCRIPTION: SEQ ID NO. 91: Arg Glu Asp Ala Leu Thr Ser His Glu Arg
5 <u>∠2|0></u> <del>(2) INFORMATION FOR SEQ ID NO+</del> 92: (1) GEQUENCE CHARACTERISTICS (2) (A) LENGTH+ 10 amino acide PKT (C) STRANDEDNESS+ -(D) TOPOLOGY - unknown --(ii) MOLECULE TYPE: peptide -∠400> (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92: Arg Val Asp Ala Leu Glu Ala His Arg Arg ∠2/0> (2) INFORMATION FOR SEQ ID NO+ 93: (1) SEQUENCE CHARACTERISTICS+

(2) (2) LENGTH: 10 amino acide

(3) TYPE: amino acid PRT

(4) STRANDBORGES: (D) TOPOLOGY: unknown (ii) MOLEGULE TYPE: poptide \_\_ (x1) SEQUENCE DESCRIPTION: SEQ 10 NO. 93: Asp Arg Ser Ser Leu Thr Arg His Thr Arg 5 ≤≥|0> -(2) INFORMATION FOR SEQ ID NO: 94: (i) SEQUENCE CHARACTERISTICS:

[2] - (A) LEMOTH: 10 amino acid.

[B] TYPE: amino acid. P/(C) STRANDEDNESS:

(C) TOPOLOGY: unknown -(ii) MOLBCULE TYFE: -peptido -∠400> (\*4) SEQUENCE -DESCRIPTION - SEQ. ID NO. 94: Glu Arg Thr Ser Leu Ser Arg His Ile Arg ∠2/0 > <del>(2) INFORMATION FOR SEQ ID NO.</del> 95: (i) CEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 mino acide

(B) TYPB: amino acid PRT

(C) STRANDEDNESS:

(B) TOPOLOGY: unknown (ii) MOLECULE TYPE: peptide U[GO > -(x1) SEQUENCE DESCRIPTION: SEQ ID NO+ 95: Gly Ala Arg Ser Leu Thr Arg His Gln Arg 5 ∠2/0> (2) INFORMATION FOR SEQ ID NO+ 96: (1) SEQUENCE CHARACTERISTICS |
21|> (A) LENGTH: 10 amino solds
21|2> (B) TYPE+ amino sold PRT
(C) STRANDEDNESS. (D) TOPOLOGY + unknown

(ii) MOLEGULE TYPE: poptide ...

∠UOO> -(x±)-GEQUENCE-DESCRIPTION+ GEQ\_ID-NO+-96: Thr Gly Gly Ser Leu Ala Arg His Glu Arg 5 ∠∠(0> -(2) ENFORMATION POR CEQ ID NO. 97: (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acid
(2) (B) TYPE: amino acid STRANDEDNESS 1 (D) TOPOLOGY: unknown (11) MOLECULE TYPE: peptide-(\*4) SEQUENCE DESCRIPTION: SEQ 15 NO+ 97: Gln Arg Ala Ser Leu Ala Ser His Met Arg
5 10 (1) SEQUENCE CHARACTERISTICS:
(2) (R) LENGTH: 10 cartno acids
(B) TYPE: anino acid PRI
(C) STRANDEDNESS: (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: poptide 400> (wi) SEQUENCE DESCRIPTION: SEQ ID NO. 98: Asn Arg Asp Thr Leu Thr Arg His Ser Lys
5 10 ∠2/0> -(2) INFORMATION FOR SEQ IS NO. 99: (1) SEQUENCE CHARACTERISTICS: (2) STRANDEDNESS: -(D) TOPOLOGY: unknown (ii) MOLECULE TYPE - poptide. ∠400> -(xi-)-SEQUENCE-DECORIPTION: SEQ ID NO. 99: Glu Arg Gly Thr Leu Ala Arg His Glu Arg 2/0> (3) INFORMATION FOR SEQ ID NO: 100: (1) SEQUENCE CHARACTERISTICS:

| A) LENGTH: 10 amino acide
| A) TYPE - amino acide | PK |
| (C) STRANDEDNEGO - (D) TOPOLOGY - unknown -(ii) MOLECULE TYDE: poptido ∠400> (x1) SEQUENCE DESCRIPTION: SEQ ID NO. 100: Arg Gly Asp Ala Leu Thr Ser His Glu Arg 5 10 <u>∠2|0>-(2) INFORMATION FOR SEQ ID NO+-</u>101: (1) SEQUENCE CHARACTERISTICS: (3) TYPE: amino acide PRT

(ii) MOLECULE TYPE: paptide

(D) TOPOLOGY: unknown

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-continued
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∠400> -(xi) GEQUENCE DESCRIPTION: SEQ TO NO: 101: Arg Ala Asp Ala Leu Met Val His Lys Arg ∠≥(0> 12) INFORMATION FOR SEQ ID NO. 102: (1) EEQUENCE CHARACTERISTICS: (C) STRANDEDNEGG+ -(B) TOPOLOGY: unknown (11) MOLECULE TYPE: poptide ∠400> -(\*±)- GEQUENCE DESCRIPTION: GEQ ID NO: 102: Arg Gln Asp Thr Leu Val Gly His Glu Arg ∠ 2/D > CONTROL TO THE SECULO NO + 103: (1) - SEQUENCE CHARACTERISTICS: (a) LEBETH: 10 anino soide PRT (b) TOPOLOGY: unknown -(11) -MOLECULE TYPE: poptide (LOO) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103: Arg Gln Ser Thr Leu Val Arg His Thr Arg
5 10 ∠≥|Ø> -(2) INFORMATION FOR SBQ ID NO+ 104: (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10-amino coid

(B) TYPE: amino acid

(C) STRANDEDNESS: \_(D)\_TOPOLOGY:-unknown -(ii) MOLECULE TYPE: peptide <u>∠460>-(xi)-sequence-description-seq\_id\_No+</u>104: Arg Ala Ala Asp Leu Asn Arg His Val Arg <u>∠210></u> <del>(2) INFORMATION FOR SEQ ID NO+</del> 105: (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acida

(B) TYPET amino acid

(C) STRANDEDNESCO

(D) TOPOLOGY: unknown (11) MOLEGULE TYPE: poptide (400> (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 105: Arg Lys Asp Val Leu Val Ser His Val Arg
5 (2) THEORMATION FOR SEQ ID NO. 106: -SEQUENCE-CHARACTERISTICS: (21) (A) LENGTH: 10 -omino aci ZIZS(B) TYPE: amino acid (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

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CHOO TELL SEQUENCE DESCRIPTION: SEQ TO NO: 106:
             Arg Arg Asp Val Leu Met Asn His Ile Arg
  ∠20> (2) INFORMATION FOR SEQ ID NO:-107:
                 (c) STRANDEDNESC+
                         -(D) TOPOLOGY: unker
                 (11) MODECULE TYPE: peptide-
      (#1) SEQUENCE DESCRIPTION: SEQ ID NO+ 107:
             Arg Ser Asp Thr Leu Lya Lya His Gly Lya
5 10
 Q10> (2) INFORMATION FOR SEQ ID NO. 108:
                 (2) CEQUENCE CHARACTERISTICS:
(2) (A) LENGTH 10 anino acido
(2) (B) TYPH anino acido PRT
(C) STRANDEDNESS:
                          (C) STRANDEDNESS:
                         (D) TOPOLOGY: unknown-
                  (ii) MOLECULE TYPE: peptide-
       ∠440> (x1) SEQUENCE DESCRIPTION: SEQ 10 NO+ 108:
             Arg Gly Pro Asp Leu Ala Arg His Gly Arg
∠2/0> (2) INFORMATION FOR SEQ ID NO. 109:
                  (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH+ 10 amino acid

(B) TYPE+ amino acid

(C) STRANDEDNESS+

(D) TOPOLOGY: unknown
                 (11) MOLECULD TYPE: peptido-
     ∠400> (*4) SEQUENCE DESCRIPTION: SEQ 10 NO: 109:
             Ala Arg Glu Val Leu Gln Arg His Thr Arg

∠2/0> (2) INFORMATION FOR CEQ ID NO+ 110:

                 (1) SEQUENCE CHARACTERISTICS:
(2) (A) LENGTH: 10 amino acids
(2) (B) TYPE: amino acid PRT
(C) STRANDEDNESS:
                         (D) TOPOLOGY+-unknown-
                 -(11) MOLECULD-TYPE: peptide
       ∠460>-(*4) SEQUENCE DESCRIPTION: SEQ ID NO: 110:
            Arg Glu Asp Val Leu Ile Arg His Gly Lys 5
∠20> -(2) INFORMATION FOR SEQ ID NO+ 111:
                 (i) esquence characteristics:

(2) (A) LENGTH: 10 sucho acids

(b) TYPE: amino acid PRT

(c) STRANDEDNESS.
                         (D) TOPOLOGY: naknown
```

(ii) - MOLECULE TYPE: peptide

/400> (mi) SEQUENCE DESCRIPTION: SEQ ID NO: 111: Arg Ser Asp Leu Leu Gln Arg His His Lys (4) SEQUENCE CHARACTERISTICS | DIT (A) LENGTH+ 10 onino acide | DRT (C) STRANDEDNESS. (D) TOPOLOGY unknown -(±±) MOLEGULE UNDE: poptide ∠460≥ (\*i) SEQUENCE DESCRIPTION: SEQ ID NO: 112: Arg Leu Asp Gly Leu Arg Thr His Leu Lys 5 10 <2/0> (2) INFORMATION FOR COQ ED NO: 113: (1) SEQUENCE CHARACTERISTICS (A) LENGTH 10 cmino acide PRT (B) CVPS - mino coid PRT (C) CFRANDEDNESS. (D) TOPOLOGY: unknow (ii) MOLECULE TYPE: poptide 400> (min) SEQUENCE DESCRIPTION SEQ ID NO. 113: Arg Gly Asp Ala Leu Thr Ser His Glu Arg ∠2(0> <del>(2) INFORMATION FOR SEQ ID NO+</del> 114: (i) SEQUENCE CHARACTERISTICS - (2) (A) LENGTH: 10 mino soid (E) TYPE: mino soid PRI (I) STEAMBRINGS (G)-STRANDEDNESS:-(D) TOPOLOGY: unknown -(14) MOLECULE TYPE: poptido-(#i) ODQUENCE-DESCRIPTION - SEQ ID-NO+ 114: Arg Ala Asp Ala Leu Met Val His Lys Arg < 2/0> (2) INFORMATION FOR SEQ ID NO: 115: (1) SEQUENCE CHARACTERISTICS: (C) STRANDEDNESS:

(D) TOPOLOGY: unknown -(11) MODECUBE-TYPE: peptide (xi) sequence - DESCRIPTION - SEQ ID NO. 115: Arg Val Asp Ala Leu Glu Ala His Arg Arg 5 10 (1) ODQUBNCE CHARACTERISTICS (2) (A) LENGTH 10 anino acids (2) (B) TYPE: amino acid PRT (C) GTRANDEDNEGG:

(11) MOLECULE TYPE: paptide.

1400> (xi) - SEQUENCE DESCRIPTION: CEQ ID NO: 116: Arg Arg Asp Val Leu Leu Asn His Ile Arg 12/0> -(2) INFORMATION FOR SEQ ID NO. 117: (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH 10 amino acido
(B) TYPB: amino acid PRI
(C) CTRANBEDNESS:
(D) TOPOLOGY: unknown (ii) MCLEGULE TYPE: poptido-∠400≥ (wi) GBQUBNOB DBCCRIPTION- SEQ ID NO+ 117: Arg Glu Asp Val Leu Ile Arg His Gly Lys 5 ∠2/0> <del>12) INFORMATION FOR SEQ ID NO.</del> 118: (1) SEQUENCE CHARACTER TOTTES - 21/7 (A) LENGTH 10 mino acids (B) TYPE oninc acid PR (11) MOLECULE TYPE: -poptide 400> (xi) SEQUENCE DESCRIPTION: SEQ ID NO. 118: Arg Ser Asp Leu Leu Gln Arg His His Lys 5 (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: endino acid PRT

(C) STRANDENDEG:

(D) TOPOLOGY: unknown (ii) HOLECULE TYPE: peptide LHOON (mi) SEQUENCE DESCRIPTION: SEQ ID NO: 119: Lys Ala Ser Asn Leu Val Ser His Ile Arg
5 10 ∠<u>}|0> +2) - INFORMATION FOR SEQ. ID</u> NO: 120: (#) CEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TIPB: cmine-soid

(C) CTRANDEDNESC:

(B) TOPOLOGY: unknown (11) NOLEGULE TYPE: poptide -(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120: Leu Arg His Asn Leu Glu Thr His Met Arg ∠20> 12) INFORMATION FOR CEQ ID NO. 121: ZIZA; LENGTH: 10 base pairs

ZIZA; LENGTH: 10 base pairs

ZIZA; LENGTH: 10 base pairs

(c) STRANDEDNESS: single

<u><400></u>

(xi) SEQUENCE DESCRIPTION - SEQ ID NO: 121:

(D) TOPOLOGY: Linear

-continued CGCAGAAGCC 10 ∠210> <del>(2) INFORMATION FOR SEQ ID NO.</del> 122: GEQUENCE-CHARACTERISTICS ( (A) LENGTH: 10 base pairs STRANDEDNESS: cingle TOPOLOGY: Lin ∠400> (xi) SEQUENCE DESCRIPTION SEQ ID NO+ 122: TCCAGAAGCC 10 (2)0> (2) INFORMATION FOR SEQ ID NO. 123: SEQUENCE-CHARACTERISTICS 2/1> (A) LENGTH: 10 base pairs (B) TYPB: nucleic (C) STRANDEDNESS - sing) TOPOLOGY: Linear 4400> (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123: CGCAGGTGAG 10 (3) INFORMATION FOR SEQ ID NOT 124: **4210>** GTRANDEDNESS: (D) TOPOLOGY - unkn (ii) MOLECULE TYPE: peptide 400> -(x1) GEQUENCE DESCRIPTION: GEQ ID NO. 124: Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn 5 ∠≥10≥ (2) INFORMATION FOR SEQ TO NO: 125: SEQUENCE CHARACTERISTICS! - LENGTH: 7 amino acid TYPE: amino acid PRT <del>(D)</del> STRANDEDNESS: (D) TOPOLOGY: unkn (ii) MOLECULE TYDE: poptide ∠400> (\*i) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

We claim:

1. A library of DNA sequences, each sequence encoding a zinc finger polypeptide for display, the zinc finger polypeptide comprising at least one zinc finger having partially randomised allocation of amino acids, the partially randomised selection of amino acids, the partially randomised selection of amino acids, the partially randomised selection of amino domised zinc finger having a random allocation of amino acids at positions -1, +2, +3 and +6 and at least one of positions +1, +5 or +8, position +1 being the first amino acid in the a-helix of the zinc finger.

2. A library according to claim 1, wherein the partially randomised zinc finger has random allocation of amino acids

at each of positions +1, +5 and +8.

Pro Lys Lys Lys Arg Lys Val

3. A library according to claim 1, wherein the encoded partially randomised zinc finger comprises the zinc finger of the Zif 268 polypeptide.

4. A library according to claim 1 as a fusion with a DNA 65 steps of: sequence encoding the minor coat protein of bacteriophage

- 5. A method of designing a zinc finger polypeptide for binding to a particular target DNA sequence, comprising the steps of:
  - comparing the binding to one or more DNA triplets of each of a plurality of zinc finger polypeptides having a partially randomized zinc finger, the zinc finger polypeptides being encoded by a library in accordance with claim 1; and
- selecting those nucleic acid sequences encoding randomised zinc fingers which bind to the target DNA
- 6. A method of designing a zinc finger polypeptide for binding to a particular target DNA sequence, comprising the

screening against at least a portion of the target DNA sequence, a plurality of zinc finger polypeptides having

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